

AEM: PS4

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Part I. Direct Matching

1.

```
qui{
  capture program drop make_table
  program define make_table
    syntax varlist(numeric)

    matrix table1 = J(4, 8, .)
    matrix colnames table1 = `varlist'
    matrix rownames table1 = trt_mean comp_mean diff_mean diff_se

    local i = 1
    foreach var in `varlist' {

      qui ttest `var', by(treat)

      matrix table1[1, `i'] = round(r(mu_2), 0.01)
      matrix table1[2, `i'] = round(r(mu_1), 0.01)
      matrix table1[3, `i'] = round(r(mu_1)-r(mu_2), 0.01)
      matrix table1[4, `i'] = round(r(se), 0.01)

      local i = `i'+1
    }

    matrix list table1
  end
}

use "nsw_dw.dta", clear

keep if data_id == "Dehejia-Wahba Sample"

make_table age education black hispanic nodegree married re74 re75

      age  education    black  hispanic  nodegree  married      re74      re75
trt_mean  25.82    10.35     .84     .06       .71       .19    2095.57    1532.06
comp_mean  25.05    10.09     .83     .11       .83       .15    2107.03    1266.91
diff_mean  - .76    - .26    - .02     .05       .13     - .04     11.45    -265.15
diff_se    .68     .17     .04     .03       .04     .04     516.48     303.16

use "nsw_dw.dta", clear

drop if data_id == "Dehejia-Wahba Sample" & treat == 0
```

```
make_table age education black hispanic nodegree married re74 re75
```

	age	education	black	hispanic	nodegree	married	re74	re75
trt_mean	25.82	10.35	.84	.06	.71	.19	2095.57	1532.06
comp_mean	34.85	12.12	.25	.03	.31	.87	19428.75	19063.34
diff_mean	9.03	1.77	-.59	-.03	-.4	.68	17333.17	17531.28
diff_se	.78	.23	.03	.01	.04	.03	990.69	1001.91

The non-experimental comparison and treatment group are highly imbalanced across these covariates compared to the experimental treatment and control group. There are very large (and statistically significant) differences between the treatment and non-experimental comparison group that suggest that the comparison group would have much higher earnings than the treatment group.

2.

```
use "nsw_dw.dta", clear
```

```
drop if data_id == "Dehejia-Wahba Sample" & treat == 0
```

```
* Prep data sets for merge back in after matching procedure
```

```
* create id and index vars to match on
```

```
gen id = _n
```

```
gen index = _n
```

```
* rename variables to accomodate wide format created by matching
```

```
preserve
```

```
rename * *_1m
```

```
rename id_1m id
```

```
save "treat", replace
```

```
restore
```

```
preserve
```

```
rename * *_0m
```

```
rename index_0m index
```

```
save "comparison", replace
```

```
restore
```

```
nnmatch re78 treat re74 re75, keep(match_info) replace
```

re78	Coef.	Std. Err.	z	P> z	[95% Conf. Interval]
SATE	-10475.37	3936.875	-2.66	0.008	-18191.5 -2759.233

The estimated treatment effect is -10475.37. This is in the opposite direction, and much larger than experimental treatment effect.

```

use "match_info", clear

keep if treat == 1

* merge back in other covariates dropped in matching process
merge m:1 id using "treat", ///
    keepusing(age_1m education_1m black_1m hispanic_1m married_1m nodegree_1m) ///
    keep(master match) nogen

merge m:1 index using "comparison", ///
    keepusing(age_0m education_0m black_0m hispanic_0m married_0m nodegree_0m) ///
    keep(master match) nogen

* get one row per observation (from tie matches)
collapse (mean) re74_* re75_* education_* index, by(id)

* check quality of matching for re74

reg re74_0m re74_1m
    * R-squared      = 0.9977

twoway (scatter re74_0m re74_1m) (lfit re74_0m re74_1m) || ///
    function y = x, ra(re74_0m) clpat(dash)

The observations are being very well matched on re74. Regressing the matched re74 on the treatment re74
the R-Squared is 0.9977.

* check quality of matching for re75
reg re75_0m re75_1m
    * R-squared      = 0.9929

twoway (scatter re75_0m re75_1m) (lfit re75_0m re75_1m) || ///
    function y = x, ra(re75_0m) clpat(dash)

The observations are also being very well matched on re75. Regressing the matched re75 on the treatment
re75 the R-Squared is 0.9929.

```

3.

```

* check balance of education treatment and matched comparison
ttest education_1m == education_0m
    * mean(diff) -.9477146    (se) .2238233

twoway (scatter education_0m education_1m) (lfit education_0m education_1m) || ///
    function y = x, ra(education_0m) clpat(dash)

```

Education is being very poorly matched when using only the pre-treatment income variables. The mean difference between the treatment and matched education is .95 years, and is statistically significant.

4.

```

use "nsw_dw.dta", clear

```

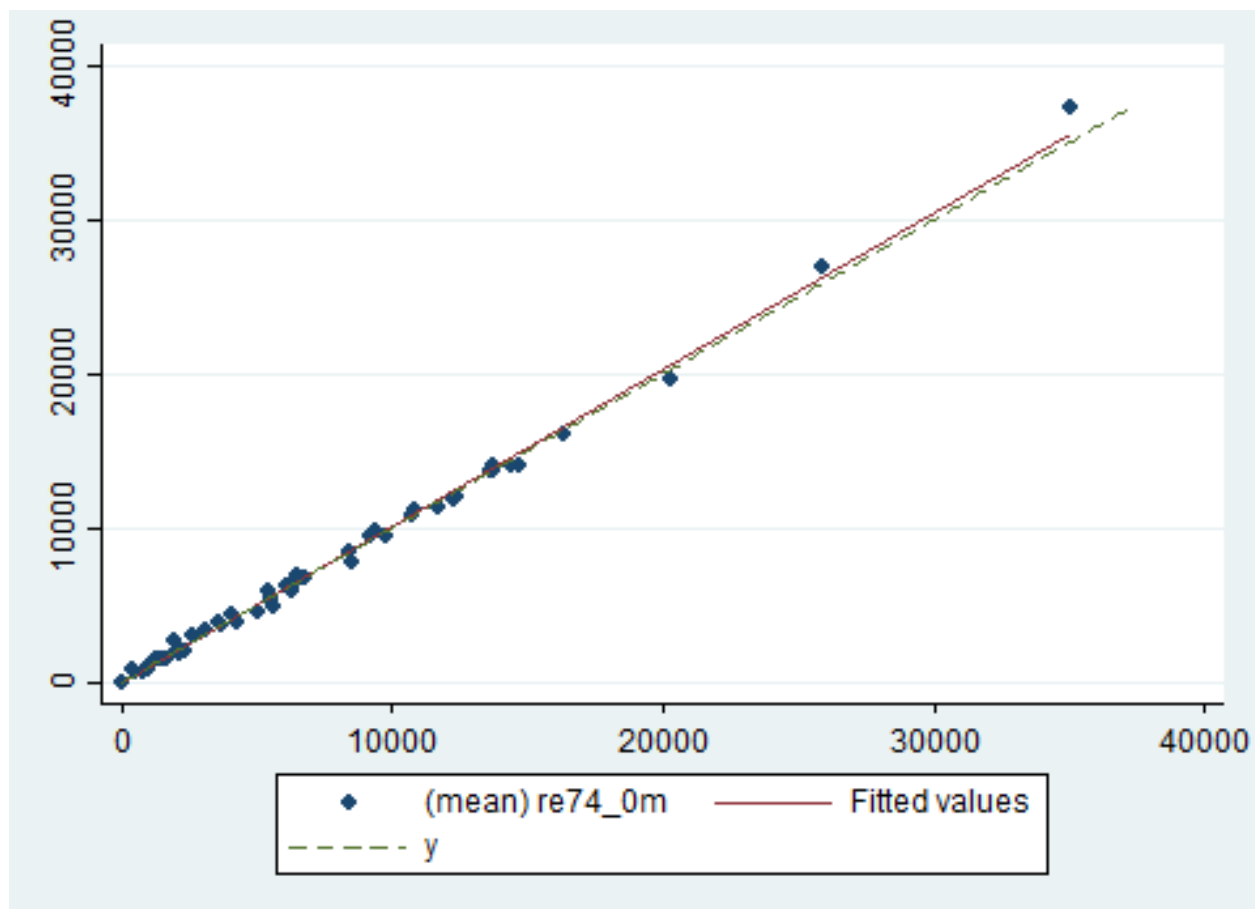


Figure 1:

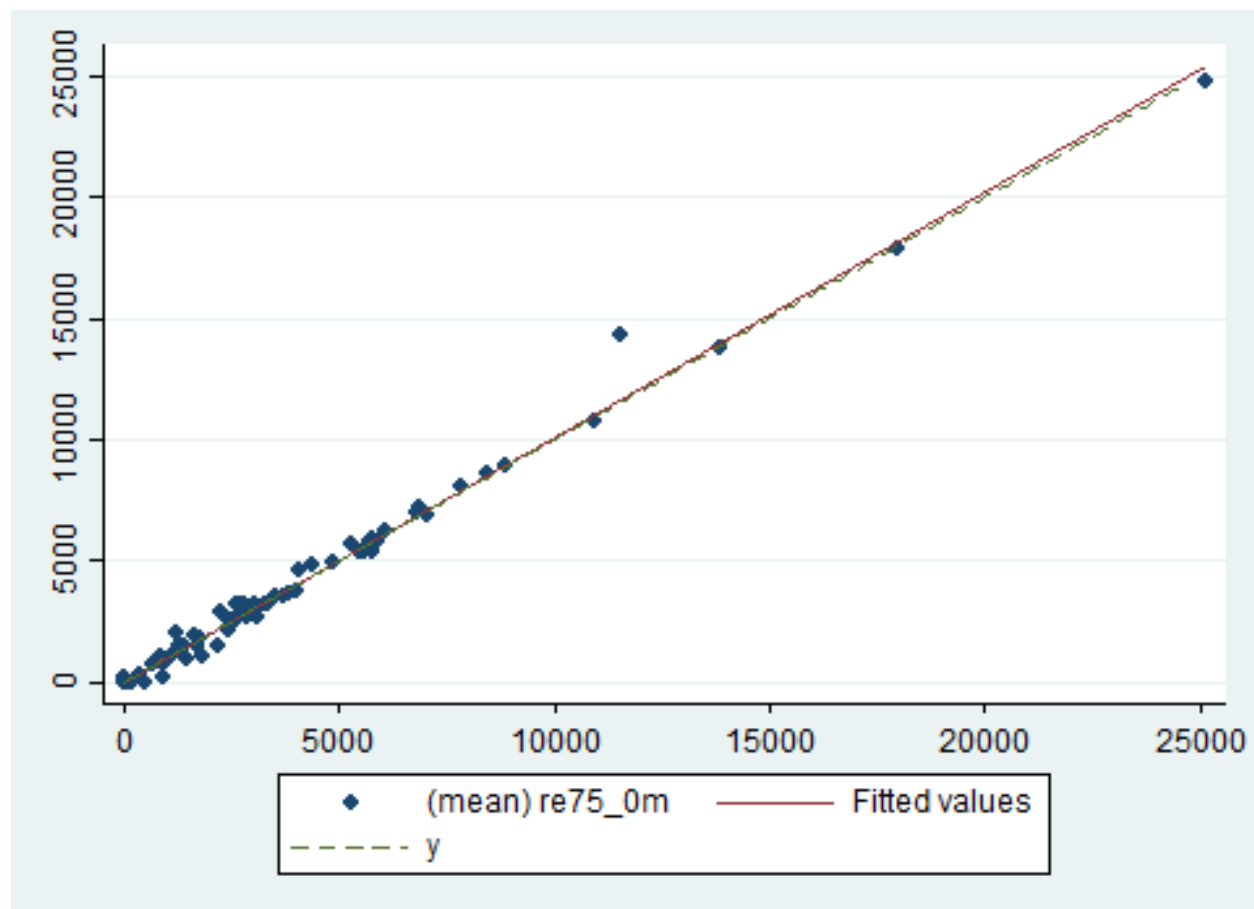


Figure 2:

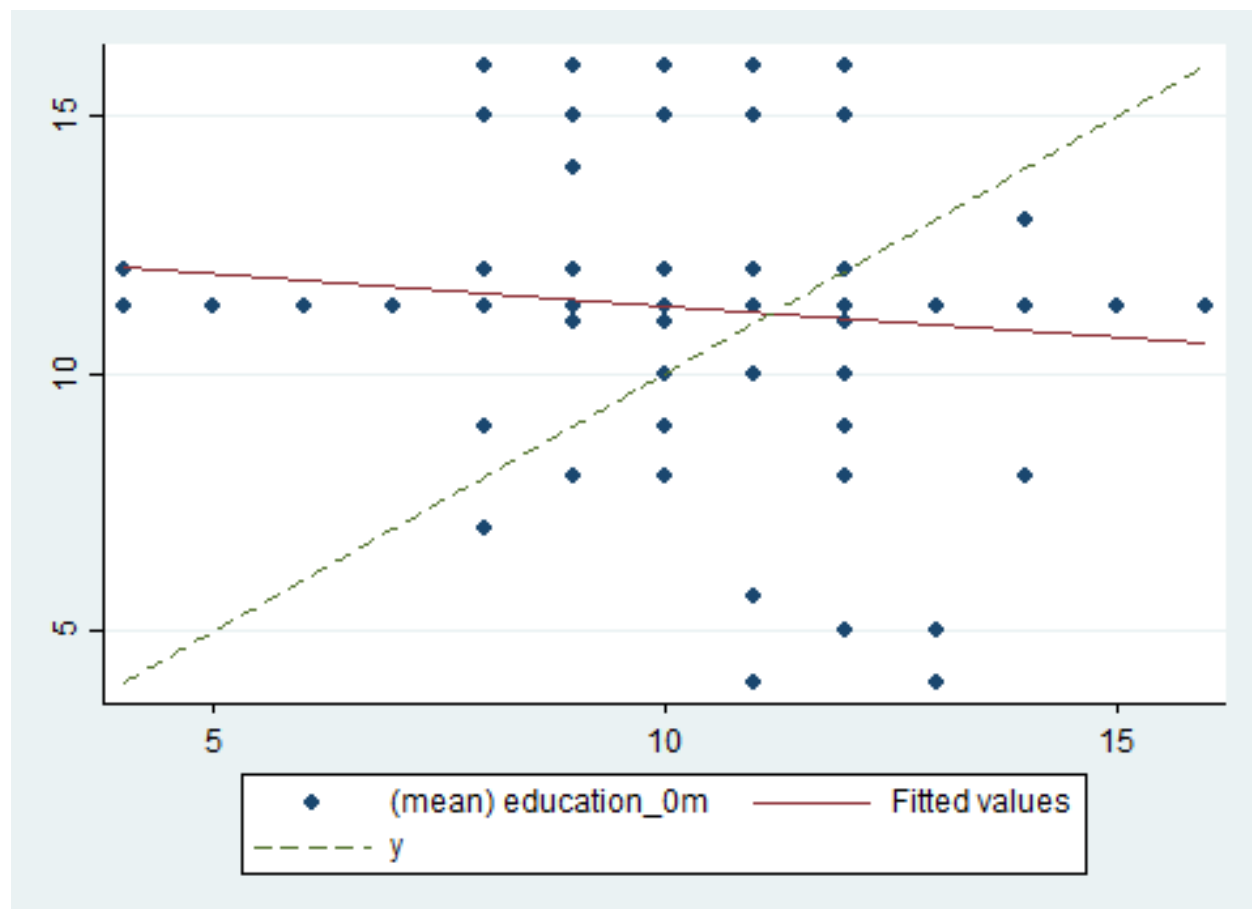


Figure 3:

```

drop if data_id == "Dehejia-Wahba Sample" & treat == 0

gen re74_sq = re74 ^ 2
gen re75_sq = re75 ^ 2

local covariates "education black hispanic married re74 re75 re74_sq re75_sq"

nnmatch re78 treat `covariates', keep(match_info2) replace

*      re78 |      Coef.   Std. Err.      z    P>|z|      [95% Conf. Interval]
*-----+-----
*      SATE | -11653.45   3990.061   -2.92   0.003   -19473.83   -3833.078

use "match_info2", clear

keep if treat == 1

* merge back in other covariates dropped in matching process
merge m:1 id using "treat", keepusing(age nodegree_1m) keep(master match) nogen

merge m:1 index using "comparison", keepusing(age nodegree_0m) keep(master match) nogen

drop re74 re75 re74_sq re75_sq
local collapse_vars = "treat re78_* age_* education_* black_* hispanic_* nodegree_* married_* re74_* re75_*"

collapse (mean) `collapse_vars', by(id)

local vars "age education black hispanic nodegree married re74 re75"

matrix table1 = J(3, 8, .)
matrix colnames table1 = `vars'
matrix rownames table1 = trt_mean comp_mean diff_se

matrix list table1

local i = 1
foreach var in `vars' {

    qui ttest `var'_0m == `var'_1m

    matrix table1[1, `i'] = round(r(mu_2), 0.01)
    matrix table1[2, `i'] = round(r(mu_1), 0.01)
    matrix table1[3, `i'] = round(r(se), 0.01)

    local i = `i'+1
}

* Assess the quality of the matches for each covariate
matrix list table1

*      age  education  black  hispanic  nodegree  married      re74      re75
* trt_mean  25.82     10.35   .84     .06     .71     .19  2095.57  1532.06
* comp_mean  29.34     10.3   .84     .06     .71     .19  2521.42  1712.76

```

```
* diff_se      .82      .03      0      0      0      0      113.68      114.88
```

The matched comparison group is now much better matched with the treatment group across these covariates, however the comparison group is still more than 3 years older on average, and makes more than \$400 more than the treatment group in 1974.

```
ttest re78_1 == re78_0
```

```
*          |          Mean  Std. Err.
* re78_1 | 6349.144   578.4229
* re78_0 | 4951.368   557.107
*-----+-----
* diff   | 1397.775    777.192
```

```
* Ha: mean(diff) != 0
* Pr(|T| > |t|) = 0.0737
```

```
use "nsw_dw.dta", clear
keep if data_id == "Dehejia-Wahba Sample"
ttest re78, by(treat)
```

```
* Experimental treatment effect estimate
* -----
```

Group	Obs	Mean	Std. Err.	Std. Dev.	[95% Conf. Interval]	
Control	260	4554.801	340.0931	5483.836	3885.102	5224.501
Treated	185	6349.144	578.4229	7867.402	5207.949	7490.338
diff		-1794.342	632.8534		-3038.11	-550.5745

```
Ha: diff != 0
Pr(|T| > |t|) = 0.0048
```

The estimated treatment effect using the matching method is 1397.78 while experimental treatment effect estimate is 1794.34.

Part II. Propensity Score Matching

5.

```
use "nsw_dw.dta", clear

drop if data_id == "Dehejia-Wahba Sample" & treat == 0

gen re74_sq = re74 ^ 2
gen re75_sq = re75 ^ 2

local spec_5_vars "education black hispanic married re74 re75 re74_sq re75_sq"
```



```

qui logit treat `spec_5_vars'

predict p_score

save "spec_5", replace

psgraph, t(treat) p(p_score)

```

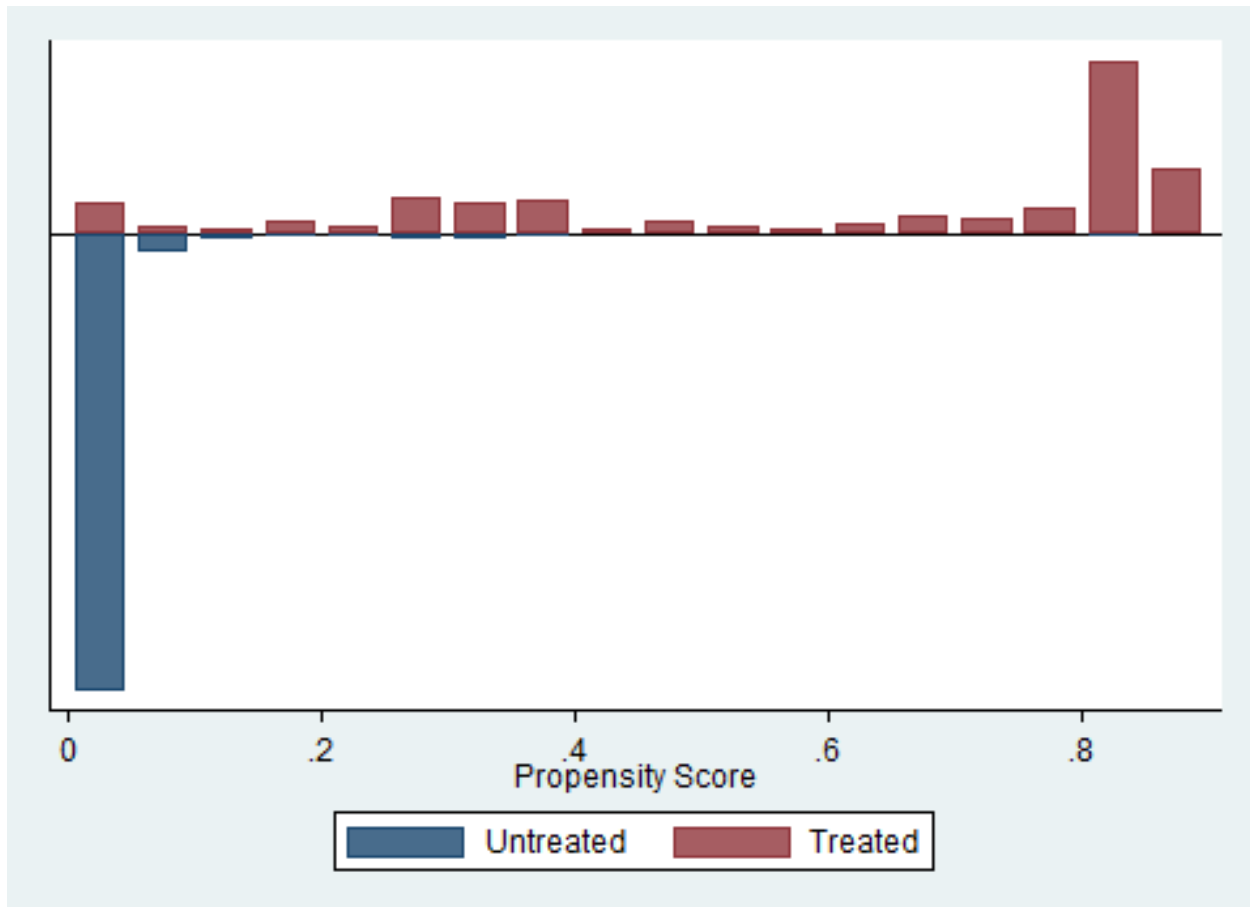


Figure 4:

```

* randomize sort of dataset so ties are matched at random
set seed 20161206
gen u = uniform()
sort u

psmatch2 treat, pscore(p_score) outcome(re78) neighbor(1) ate

local covariates "age education black hispanic nodegree married re74 re75"

pstest `covariates'

```

/*

Variable	Mean		%bias	t-test		V(T)/ V(C)
	Treated	Control		t	p> t	

age	25.816	28.627	-31.4	-3.09	0.002	0.50*
education	10.346	10.605	-10.0	-1.09	0.275	0.63*
black	.84324	.84324	0.0	-0.00	1.000	.
hispanic	.05946	.04865	5.2	0.46	0.647	.
nodegree	.70811	.56757	30.7	2.84	0.005	.
married	.18919	.15676	8.8	0.82	0.411	.
re74	2095.6	1920.3	1.7	0.40	0.693	1.91*
re75	1532.1	1832.1	-3.0	-0.81	0.421	0.68*

*/

The covariates are very well balanced for everything except **age** and **nodegree**, where the comparison group is older and more likely to have a degree. Both of these differences are statistically significant.

6.

* Propensity score matched treatment effect estimate

Variable	Sample	Treated	Controls	Difference	S.E.	T-stat
re78	Unmatched	6349.1435	21553.9209	-15204.7774	1154.61433	-13.17
	ATT	6349.1435	4584.23534	1764.90816	1902.95748	0.93
	ATU	21553.9209	6107.88894	-15446.032	.	.
	ATE			-14255.7427	.	.

* Experimental treatment effect estimate

Group	Obs	Mean	Std. Err.	Std. Dev.	[95% Conf. Interval]	
Control	260	4554.801	340.0931	5483.836	3885.102	5224.501
Treated	185	6349.144	578.4229	7867.402	5207.949	7490.338
diff		-1794.342	632.8534		-3038.11	-550.5745

Propensity score matched treatment effect estimate is 1764.91 while the experimental treatment effect estimate is 1794.34, so this matching method is working extremely well.

7.

Given that the matches in the above specification were not well ballanced for **age** and **nodegree** it's possible that the propensity score specification can be improved by adding these variables. Below I estimate the propensity score with all the variables from the previous specification and add age, age-squared, no degree, and an interaction term for education and nodegree.

use "nsw_dw.dta", clear

```

drop if data_id == "Dehejia-Wahba Sample" & treat == 0

gen re74_sq = re74 ^ 2
gen re75_sq = re75 ^ 2
gen age_sq = age ^ 2
gen educ_nodegree = education*nodegree

local spec_7_vars "age age_sq education black hispanic nodegree educ_nodegree married re74 re75 re74_sq"

qui logit treat `spec_7_vars'

predict p_score

save "spec_7", replace

psgraph, t(treat) p(p_score)

```

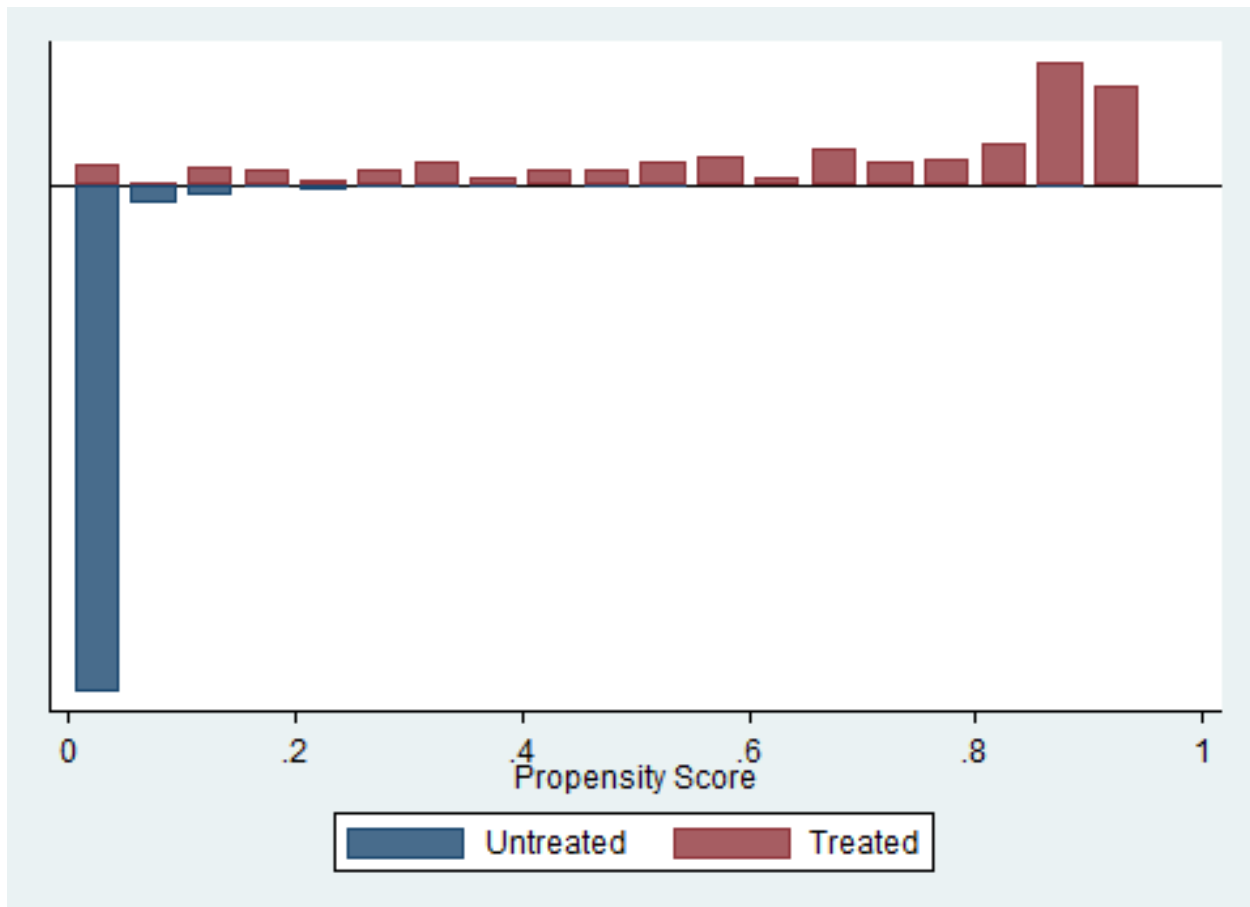


Figure 5:

```

* randomize sort of dataset so ties are matched at random
set seed 20161206
gen u = uniform()
sort u

psmatch2 treat, pscore(p_score) outcome(re78) neighbor(1) ate

```

local covariates "age education black hispanic nodegree married re74 re75"

pstest `covariates'

Variable	Mean		%bias	t-test		V(T)/ V(C)
	Treated	Control		t	p> t	
age	25.816	25.827	-0.1	-0.02	0.988	1.24
education	10.346	10.184	6.2	0.75	0.453	0.88
black	.84324	.87027	-6.7	-0.74	0.459	.
hispanic	.05946	.04865	5.2	0.46	0.647	.
nodegree	.70811	.6973	2.4	0.23	0.821	.
married	.18919	.12432	17.6	1.72	0.087	.
re74	2095.6	2397.7	-3.0	-0.68	0.495	1.94*
re75	1532.1	2046	-5.2	-1.63	0.105	1.28

This new specification achieves much better balance across all the covariates. Now there are no significant differences between the treatment and comparisons groups on any of these covariates.

* Propensity score matched treatment effect estimate

Variable	Sample	Treated	Controls	Difference	S.E.	T-stat
re78	Unmatched	6349.1435	21553.9209	-15204.7774	1154.61433	-13.17
	ATT	6349.1435	5494.63469	854.50881	1299.69314	0.66
	ATU	21553.9209	6593.604	-14960.3169	.	.
	ATE			-13866.5813	.	.

* Experimental treatment effect estimate

Group	Obs	Mean	Std. Err.	Std. Dev.	[95% Conf. Interval]	
Control	260	4554.801	340.0931	5483.836	3885.102	5224.501
Treated	185	6349.144	578.4229	7867.402	5207.949	7490.338
diff		-1794.342	632.8534		-3038.11	-550.5745

Despite the apparently improved balance of covariates, the estimated treatment effect is now only 854.51, which is much lower than the experimental treatment effect of 1794.34, so it seems the matching has not actually improved the estimate relative to the experiment.

Part III. Propensity Score Weighting

8.

```
use "nsw_dw.dta", clear

drop if data_id == "Dehejia-Wahba Sample" & treat == 0

gen re74_sq = re74 ^ 2
gen re75_sq = re75 ^ 2
gen age_sq = age ^ 2
gen educ_nodegree = education*nodegree

local spec_5_vars "education black hispanic married re74 re75 re74_sq re75_sq"

qui logit treat `spec_5_vars'

predict p_score

gen ipw_ate = re78 * ((treat - p_score) / (p_score * (1 - p_score)))
qui sum ipw_ate
di r(mean)
* -8780.056

gen ipw_att = re78 * ((treat - p_score) / ((1 - p_score)))
qui sum ipw_att
di (1 / (185 / 2675)) * r(mean)
* 2167.4583

reg re78 treat `spec_5_vars' [pweight = p_score]

drop p_score ipw_ate ipw_att
```

```
-----
            |               Robust
            |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-----+-----
    treat |      431.7796   817.8577     0.53   0.598    -1171.918     2035.477
-----
```

```
local spec_7_vars "age age_sq education black hispanic nodegree educ_nodegree married re74 re75 re74_sq"

qui logit treat `spec_7_vars'

predict p_score

gen ipw_ate = re78 * ((treat - p_score) / (p_score * (1 - p_score)))
qui sum ipw_ate
di r(mean)
* -5543.2366

gen ipw_att = re78 * ((treat - p_score) / ((1 - p_score)))
```

```

qui sum ipw_att
di (1 / (185 / 2675)) * r(mean)
* 1120.4267

```

```

reg re78 treat `spec_7_vars' [pweight = p_score]

```

		Robust				
re78		Coef.	Std. Err.	t	P> t	[95% Conf. Interval]

treat		1450.125	930.4046	1.56	0.119	-374.2643 3274.514

The average treatment effect on treated estimated via inverse propensity score weighting is 2167.46 using the first specification and 1120.43 using the second specification with additional covariates added to the estimation of the propensity score.